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UNITED STATES DISTRICT COURT

NORTHERN DISTRICT OF CALIFORNIA

SAN FRANCISCO DIVISION

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| UNITED STATES OF AMERICA,<br><br>Plaintiff,<br><br>v.<br><br>ESAU FERDINAND,<br><br>Defendant. | CASE NO. CR 13-764 WHO<br><br>GOVERNMENT'S OPPOSITION TO DEFENDANT FERDINDAND'S MOTION TO EXCLUDE DNA EVIDENCE |

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Defendant Ferdinand's motion raises very little to which the government can respond. His motion simply reasserts the conclusions reached by the analysts at SERI and suggests that there are "questions" these conclusions raise. However, he makes no specific challenge to SERI's methodology. His motion exclude DNA evidence is styled as a *Daubert* motion, but none of Ferdinand's arguments challenge the methods or principles used to obtain that evidence. Ferdinand does not challenge the scientific method used in this case – the PCR/STR process – to extract, quantify, amplify and type the biological evidence recovered from a baseball cap and a vehicle. Nor does he argue that the application of that otherwise valid method was so skewed in this case as to threaten the method itself. Ferdinand challenges only the manner in which the government's expert, Gary Harmor and Casseday Baker, interpreted the data and, in particular, the manner in which Baker reported the probability that someone else might have had the same DNA profile as that in the material found on the baseball cap and in the vehicle tested. Even taken at face value, Ferdinand's arguments all challenge Harmor and Baker's conclusions, not the principles and methods SERI used to reach those conclusions. Ferdinand thus invites the Court to leap past its "gatekeeping" function and become a fact finder. None of the issues Ferdinand raises merit a hearing, much less exclusion of the DNA evidence. Ferdinand will have the opportunity to cross-examine both Harmor and Baker and, if he chooses, put his own expert on the stand to offer competing conclusions.

Indeed, defendant Ferdinand has admittedly retained his own DNA expert— Professor Keith Inman. Yet he has not provided any declaration from that expert. He has not provided Professor Inman's opinions to the government in discovery—as he was required to do on December 15, 2015. In fact, to date the only disclosure the government has received from defendant Ferdinand concerning Professor Inman is his CV. Finally, the defendant has not cited to a single opinion where a court found the methodology SERI used in this case to be unreliable. The Court should deny the motion.

## I. BACKGROUND

### A. Case Background

Jelvon Helton—brother of CDP victim Andre Helton—was shot and killed at close range at Gravity Bar in San Francisco in November 2010. Jaquain Young has been charged with Jelvon Helton's murder. Defendant Ferdinand is an accomplice to the murder. He was present with Young at Gravity Bar and present with Young when he fled the scene following with murder in Young's Acura vehicle.

Defendant Williams was also present, but left in a separate vehicle. At the scene of the homicide, law enforcement seized a baseball cap near Helton's body and swabbed it for DNA. They also swabbed defendant Young's Acura for DNA.

On May 26, 2015, the government produced in discovery reports regarding DNA testing performed by Serological Research Institute ("SERI") and relevant to defendant Ferdinand. As stated in the government's October 21, 2015 expert disclosure, Gary Harmor and Casseday Baker of SERI will testify in the following manner consistent with their reports:

We also currently anticipate that Harmor will testify to the following conclusions reflected in the M'9850'14 report:

- "The genetic marker profile obtained from the back inside dome swabbing of the red baseball cap # I B 11 5 (item 3C) is a mixture from at least three individuals Jelvon Helton # I B2 19 could be a major contributor to this mixture. The chance someone unrelated to him could also be the major contributor is approximately one in 13 sextillion. Esau Ferdinand # I B232 could be a minor contributor to the mixture as well as approximately one in 12 persons with relationship to him."
- "The genetic marker profile obtained from the rear sweatband swabbing of the red baseball cap # I B lI S (item 3B) is a mixture from at least three individuals. Jelvon Helton #1 B219 could be a major contributor to this mixture as well as approximately one in 6170 persons. Esau Ferdinand # I B232 could be a minor contributor to the mixture. Approximately one in every 55 individuals could also be contributors to the mixture with relationship to Esau Ferdinand.
- "The genetic marker profile obtained from the front sweatband swabbing of the red baseball cap # I B lIS (item 3A) is a mixture from at least three individuals. Jelvon Helton # IB2 19 (item 1-1 , SERI Case No. M'9851'14) could be a possible contributor to this mixture as well as approximately one in 59,000 persons. Esau Ferdinand # I B232 (item 4A-I) and Vernon Carmichael # 1 B218 ( item 2A-1. SERI Case No. M'9852'14) could be minor contributors to the mixture. Approximately one in every 9 individuals could also be contributors to the mixture with relationship to Ferdinand and Carmichael."

We currently anticipate that Baker will testify to the following conclusions reflected in the M'9851'14 report:

- "DNA recovered from the steering wheel swab (item 2-2) is a mixture of at least four people. Esau Ferdinand and Vernon Carmichael are each included as possible contributors to the mixture. The chance that a randomly selected person, unrelated to Esau Ferdinand and Vernon Carmichael would be similarly included as a possible contributor is one in ten. Jaquain Young is also included as a possible contributor. The chance that a randomly selected person, unrelated to Jaquain Young would be similarly included as a possible contributor is one in six hundred sixty."

"DNA recovered from the front passenger handle swab (item 2-3) is a mixture of at least three people. Esau Ferdinand is included as a possible contributor to the mixture. The chance that a randomly selected person, unrelated to Esau Ferdinand, would be similarly included is about one in two hundred eighty. Vernon Carmichael is also included as a possible contributor. The chance that a randomly selected person, unrelated to Vernon Carmichael, would be similarly included as a contributor is about one in eleven."

- "DNA recovered from the rear driver carpet stain (item 5) is a mixture of at least three people. Jaquain Young is included as a possible contributor to the mixture. The chance that a randomly selected person, unrelated to Jaquain Young, would be similarly included as a contributor is about one in three thousand. Vernon Carmichael is also included as a possible contributor to the mixture.

> The chance that a randomly selected person, unrelated to Vernon Carmichael, would be similarly included as a contributor is about one in forty-eight."

Ferdinand seeks to exclude that evidence.

**B. The Serological Research Institute ("SERI")**

SERI is a private, not-for-profit laboratory that has been in existence for over 35 years. The lab is accredited by the American Society of Crime Laboratory Directors' Laboratory Accreditation Board ("ASCLD/LAB") in the areas of Biology (serology, screening, STRs, YSTRs and mitochondrial DNA). According to Ferdinand, ASCLD is an organization composed of the directors of accredited laboratories in the United States. *Rudin & Inman, Intro. to Forensic DNA Analysis*, at 175-76. ASCLD establishes standards for the management and operation of crime labs and for the education and proficiency testing of lab workers. *Id.* ASCLD conducts regular inspections to ensure that labs seeking accreditation or reaccreditation are performing according to the standards ASCLD sets, and that the labs have protocols in place to maintain that performance. *Id.* In order to remain accredited with ASCLD/LAB, a lab must undergo a full inspection once every five years. *Id.* SERI's most recent accreditation was on May 26, 2015. It remains effective until May 25, 2019. ASCLD conducted its inspection of SERI in March of 2015.

**C. Background Regarding DNA Profiling**[1]

Almost every nucleated cell in the human body contains a complete copy of that person's DNA. The DNA in each cell is identical to the DNA in all other cells. An individual's DNA resides on 23 pairs of chromosomes. One of each pair of chromosomes comes from a person's mother, the other comes from the person's father.

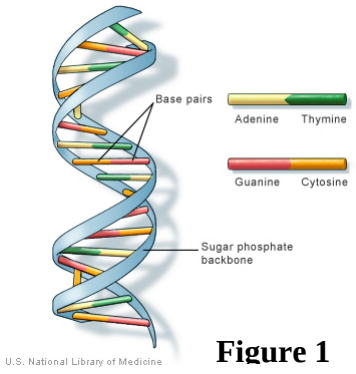


**Figure 1**

The chromosomes themselves are composed of twin strands of sugar-phosphates linked together by nitrogenous bases. If stretched out flat, the chromosome would look like a ladder, where the sugar-

[1] The following summary is drawn from the National Research Council's "The Evaluation of Forensic DNA Evidence," (1996) at 12-14 and 60-74, as well as *United States v. Davis*, 602 F. Supp. 2d 658, 663-67 (D. Md. 2009), *United States v. Ewell*, 252 F. Supp. 2d 104, 107-109 (D.N.J. 2003) and *United States v. Trala*, 162 F. Supp. 2d 336, 339-344 (D. Del. 2001), all of which found PCR/STR testing to be a reliable methodology.

phosphates were the sides and the nitrogenous bases were the rungs. In fact, this ladder is coiled up into a structure called a "double helix," as depicted in Figure 1. There are four nitrogenous bases in the double helix: adenine ("A"), guanine ("G"), thymine ("T") and cytosine ("C"). The bases A and T pair together, as do G and C. Thus, if one strand has the bases A-G-A-T, the complementary strand will have the bases T-C-T-A. The nitrogenous base link between the two strands is called a "base pair." Thus, for example, the link between A on one strand and T on the opposing strand is a base pair. The sequence A-G-A-T, which links with T-C-T-A on the opposing strand, is four base pairs. There are approximately 3 billion base pairs total on the 23 pairs of chromosomes.

DNA analysts have identified specific locations on 15 of the 23 chromosome pairs that are known as "Short Tandem Repeats," or "STRs." STRs are multiple copies of the same base pair sequence in direct succession. Thus, one of the STRs used in this case, known as CSF1PO, is found on Chromosome 5. CSF1PO is comprised of the base-pair sequence A-G-A-T. Everyone has CSF1PO. Further, CSF1PO is "polymorphic," which means that there are different forms of CSF1PO. Each form is called an "allele." The different alleles vary in the number of times the A-G-A-T sequence is repeated. Thus, allele #5 has 5 repetitions of the A-G-A-T sequence: A-G-A-T-A-G-A-T-A-G-A-T-A-G-A-T-A-G-A-T. Another allele has 6 repetitions. There are 23 alleles for CSF1PO, and they range in size from 5 to 15 repetitions. Different persons may have different CSF1PO alleles. Moreover, since Chromosome 5 is actually a pair of chromosomes, each person has two copies of CSF1PO, one on each chromosome in the pair. And since one copy is inherited from the father and one is inherited from the mother, a person may have two copies of the same allele ("homozygous") or two different alleles ("heterozygous") at that locus.

Population geneticists have studied the frequency with which each STR occurs in a particular population. Using that information, a forensic scientist can estimate the rarity of the particular combination of alleles that a person possesses. The scientist expresses that conclusion as a probability that an unrelated person would have the same DNA profile as the sample.

**D. The PCR/STR DNA Typing Method**

SERI conducted its forensic DNA analysis using the PCR/STR method.[2] The PCR/STR method

[2] Ferdinand states in his motion that "If a large quantity of high quality DNA has been extracted, 'RFLP'

is comprised of five general steps: (1) extraction, (2) quantification, (3) amplification, (4) electrophoresis and, (5) interpretation.

**1. Extraction**

In the first step, the scientist separates the genetic material in a sample from the rest of the biological material and then purifies the genetic material. In this case, Baker processed three sets of samples. Those samples were taken from: (a) the CHP's swabs of the.25 cal. pistol; (b) Baker's swabs of the.25 cal. pistol; and, (c) Bakers swabs from the .357 cal. revolver.

**2. Quantification**

In the second step, the scientist measures the amount of genetic material present in the sample. The results typically are measured in nanograms (billionth of a gram) or picograms (trillionth of a gram). The quantification step helps the scientist determine whether any analysis is possible and, if so, how to amplify the material for analysis.

**3. Amplification**

During this stage of the process, the scientist increases the number of copies of specific parts of the genetic material to be used in the subsequent typing – in this case, 15 STRs. The scientist uses a kit – in this case, Applied Biosystems' Identifiler Plus kit – containing enzymes and primers that are designed to bind to and amplify those STRs. Those 15 loci – 13 of which are considered the "core CODIS" loci[3] – are chosen because they are polymorphic, thereby enabling the resulting DNA profile to discriminate between different persons. The process the kit uses to amplify the STRs is the polymerase

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testing can be utilized to produce a 'match' between the evidence DNA and the DNA from a known sample. Motion at 4-5. If only a minute quantity of DNA is extracted or that DNA is old or degraded, RFLP testing is not possible and 'PCR/STR' testing can be utilized to develop a DNA profile." Mot. at 3. This is misleading. While it is true that RFLP testing requires larger quantities of genetic material, and that PCR/STR testing effective with smaller quantities and even with degraded samples, it is not the case that a scientist today would choose the PCR/STR test because the sample was small or degraded. To the contrary, the greater sensitivity and resilience of PCR/STR testing is the reason it has become the standard in the forensic community, and why RFLP testing has become obsolete. *See, e.g., People v. Nelson*, 43 Cal. 4th 1242, 1258 (2008). Indeed, the national CODIS system is based on PCR/STR testing, not RFLP testing. So the fact that Baker used the PCR/STR testing method says nothing about the quality of the sample. It indicates only that he was adhering to the norms in the forensic community. *See, e.g., An Introduction to Forensic DNA Analysis*, 2d ed. (2002), Rudin, N and Inman, K. at 41 ("Most laboratories today employ one of the commercially available automated short tandem repeat (STR) multiplex systems for forensic DNA typing of new case material.").

[3] CODIS is the Combined DNA Index System, a national database the FBI maintains, which contains the DNA profiles of convicted felons.

chain reaction ("PCR"). The PCR process is analogous to the process the body uses to replicate DNA naturally. It exponentially increases the number of copies of the targeted areas – the STRs.

Amplification takes place in stages. First, the two strands DNA are separated. The separated strands become the templates for the manufacture of new strands identical to the original complementary strands. Second, the single strand segments are hybridized with the specific primers contained in the kit. These primers are designed to bind to a specific sequence of base pairs adjacent to the STRs that the kit targets for amplification. The primers then facilitate the replication of that target sequence. Third, the target sequences are replicated through a process of heating and cooling. The number of heating and cooling cycles varies depending on the amount of input DNA in the sample they are amplifying. In this case, both Harmor and Baker used 29 cycles. This was consistent with the Identifiler Plus kit amplification guidelines. The kit's maker states that "[t]he Identifiler Plus Kit offers two PCR-cycle-number options," including a "[s]tandard 28-PCR-cycle protocol" for between 0.5ng to 1ng of input DNA, and a "29-PCR-cycle protocol" for 0.125-0.5ng of input DNA. Moreover, the kit maker has studied and validated that protocol and published its study in a peer-reviewed journal. See Wang, D., et al, "Developmental Validation of the AmpF*l*STR Identifiler Plus PCR Amplification Kit: An Established Multiplex Assay with Improved Performance," J. Forensic Sci. (March 2012) Vol. 57, No. 2 at 463. Also at this stage, the amplification kit attaches fluorescent markers to the replicated STR sequences during the PCR process. This enables the scientist to observe those sequences later as they pass through a laser. There are four different colors of marker: blue, green, yellow and red.

**4. Electrophoresis and Typing**

During this process, the scientist injects the extracted and amplified genetic material into a capillary tube filled with a liquid polymer. The scientist can vary the amount of genetic material injected into the capillary tube by increasing the injection time. The standard injection times are 5, 10 and 20 seconds. The electrophoresis instrument passes a weak electrical current through the capillary tube, drawing the STR fragments from one end to the other. The polymer inside the tube acts like a sieve, allowing the smaller fragments to move more quickly than the larger fragments and, thereby, separating the fragments by size. As the STR fragments reach the end of the tube, they pass by a laser which causes the fluorescent markers to light up. A computer measures the intensity of that

fluorescence and translates it into a peak on a graph, where the height of the peak indicates the intensity of the fluorescence. That, in turn, indicates the amount of material that passed through the laser at that point. The computer also determines, based on the length of time it took the STR fragments to migrate through the capillary tube and the color of the marker, which STRs and which alleles of that STR are passing through the laser at any given time. In this way, the analyst can determine not just which alleles are present, but also the relative quantities of each allele.

**5. Interpretation**

In the final step, the analyst interprets the results to determine whether a DNA profile in the sample matches a profile in a known reference. If there is a match, the analyst may apply a statistical calculation to the results to determine the significance of that match – i.e., the probability that someone other than the known reference could have contributed the DNA profile found in the evidence sample.

There are at least three different statistical models that may be used to interpret the results of a DNA test. They are the Combined Probability of Inclusion ("CPI") or its inverse the Combined Probability of Exclusion, the Random Match Probability ("RMP") and the Likelihood Ratio ("LR"). The CPI expresses the probability that a person randomly chosen from the population can be included as a contributor of the given mixture profile. The RMP expresses the probability that a particular DNA profile would be found at random among the persons in a given population. And the LR expresses the ratio of possibilities under two alternative hypotheses, often referred to often referred to as the prosecution hypothesis and the defense hypothesis.

Each statistical model has its advantages and disadvantages. The advantage of the CPI model is that it makes no assumptions about the number of contributors to a mixture and is easier to understand by someone not familiar with forensic statistical analysis. The disadvantage is that the CPI model uses less of the information available from the data. For example, it does not consider peak heights/signal intensities. For this reason, the CPI often is described as a more conservative model. The advantage of the RMP is that it makes use of peak height/signal intensity information in the identification of major and minor contributors to a mixture. The RMP thus requires an assumption about the profile of a particular contributor. The advantage of the LR is that it utilizes more information in the data than either the CPI or RMP do (including peak height/signal intensity). The disadvantage is that it requires

numerous assumptions about the prosecution and defense hypotheses of the case. This not only makes the ratio difficult to calculate – since there may be multiple hypotheses, which the analyst may not know and which may change over the course of the case – but also difficult to explain to lay persons.

There is no consensus on which statistical method to apply in a given case. Though each method has its supporters and detractors, all three are accepted ways to interpret DNA results. In 1994, the DNA Identification Act provided for the formation of a panel of distinguished professionals, from the public and private sectors, to address issues relevant to forensic DNA applications. This panel, titled the DNA Advisory Board ("DAB"), first convened in 1995. One of the DAB's early missions was to develop and implement quality assurance standards for use by forensic DNA testing laboratories. On February 23, 2000, the DAB published a paper called "Statistical and Population Genetics Issues Affecting the Evaluation of the Frequency of Occurrence of DNA Profiles Calculated from Pertinent Population Database(s)." The purpose of the paper was to assess the statistical methods used to explain the significance of a DNA profile match. The DAB wrote:

> [T]here are alternate methods for assessing the probative value of DNA evidence. Rarely is there only one statistical approach to interpret and explain the evidence. The choice of approach is affected by the philosophy and experience of the user, the legal system, the practicality of the approach, the question(s) posed, available data, and/or assumptions. For forensic applications, it is important that the statistical conclusions be conveyed meaningfully. Simplistic or less rigorous approaches are often sought. Frequently, calculations such as the random match probability [RMP] and probability of exclusion [CPE/CPI] convey to the trier of fact the probative value of the evidence in a straightforward fashion. Simplified approaches are appropriate, as long as the analysis is conservative or does not provide false inferences. Likelihood ratio (LR) approaches compare mutually exclusive hypotheses and can be quite useful for evaluating the data. However, some LR calculations and interpretations can be complicated, and their significance to the case may not be apparent to the practitioner and the trier of fact.
> . . .
> The DAB recognizes that these different approaches can be applied, as long as the question to be answered and the assumptions underlying the analyses are clearly conveyed to the trier of fact.

The Scientific Working Group on DNA Analysis Methods ("SWGDAM") reached a similar conclusion. According to Ferdinand, SWGDAM is a "forum for forensic DNA laboratories to discuss issues, conduct studies, and reach a consensus as to the DNA methodologies to be used in North American crime laboratories," and includes forensic scientists from public laboratories throughout the United States. Rudin and Inman, Intro. to Forensic DNA Analysis, at 176. SWGDAM "has played a

particularly important role in establishing guidelines for working forensic DNA laboratories." Id. According to Inman, SWGDAM has "emerged as a nucleus around which the forensic community can assemble as the DNA typing explosion continues." Id. In 2010, SWGDAM issued its "Interpretation Guidelines for Autosomal STR Typing" ("SWGDAM guidelines"), which provides:

> In forensic DNA testing, calculations are performed on evidentiary DNA profiles that are established as relevant in the context of the case to aid in the assessment of the significance of an inclusion. These calculations are based on the random match probability (RMP), the likelihood ratio (LR), or the combined probability of exclusion/inclusion (CPE/CPI).

SWGDAM Guidelines ¶ 4.

## II. ARGUMENT

### A. The *Daubert* Standard

Ferdinand styles his motion as a *Daubert* challenge to the reliability of the methods Baker used to the DNA evidence in this case. Federal Rule of Evidence 702 authorizes an expert to offer opinion testimony if that opinion is based on sufficient facts or data, is the product of reliable principles and methods, and the expert has reliably applied those principles and methods to the facts of the case. The Court acts as a "gatekeeper," ensuring that "any and all scientific testimony or evidence admitted is not only relevant, but reliable." *Daubert v. Merrell Dow Pharm.*, 509 U.S. 579, 589 (1993). The latter assessment – the reliability of the expert's methods – "entails a preliminary assessment of whether the reasoning and methodology underlying the testimony is scientifically valid and of whether that reasoning or methodology properly can be applied to the facts in issue." *Id.* at 592-93. The Court considers (1) whether the technique can be and has been tested; (2) whether the technique has been subjected to peer review; (3) the known or potential error rate and the existence of standards controlling the technique's operation; and, (4) whether the technique is generally accepted. *Id.* at 593-94.

### B. Ferdinand Does Not Challenge PCR/STR Testing or the Statistical Formulae Used.

SERI used the PCR/STR method to analyze the genetic material recovered in this case. The PCR/STR method is the standard method the forensic community uses to analyze DNA evidence and has been for over a decade. Rudin & Inman, Intro. to Forensic DNA Analysis, at 41. Scientists have studied the method and published the results of their studies in peer-reviewed journals. Id. (citing authorities). The FBI studied the error rate for this method and concluded that, when performed

properly, the error rate is zero. *Id.; Williams*, 2008 WL 5382264, at *6; *Ewell*, 252 F. Supp. 2d at 109. Numerous courts already have found that the PCR/STR method of analyzing DNA is reliable. *See, e.g.*, *United States v. Wright*, 215 F.3d 1020, 1027 (9th Cir. 2000); *United States v. Davis*, 602 F. Supp. 2d 658, 672 (D. Md. 2009); *United States v. Williams*, 2008 WL 5382264, at *15 (C.D. Cal. Dec. 23, 2008); *Ewell*, 252 F. Supp. 2d at 115-16. Ferdinand does not argue otherwise. The Court should find that PCR/STR testing is reliable.

**C. Ferdinand Questions Harmor and Baker's Conclusions, Not Their Methods.**

Rather than challenging the science underlying the PCR/STR method or the statistical models themselves, Ferdinand questions SERI's decisions about which data sets to interpret and which statistical calculations to apply to those interpretations. This is not a *Daubert* challenge. Though Rule 702 directs the Court to consider whether the expert has "reliably applied the principles and methods to the facts of the case," the focus of a *Daubert* challenge "must be solely on principles and methodology, not on the conclusions that they generate." *Daubert*, 509 U.S. at 595. The Court's role is to evaluate "the scientific validity of the expert's methods, rather than the soundness of his specific conclusions." *United States v. Trala*, 162 F. Supp. 2d 336, 344 (D. Del. 2001). Challenges to the "proficiency of the tester rather than the reliability of the test" go to the weight of the evidence, not its reliability and admissibility. *United States v. Davis*, 602 F. Supp. 2d 658, 678 (D. Md. 2009). As Ferdinand's own authorities state, "[a]n allegation of failure to properly apply a scientific principle should provide the basis for exclusion of an expert opinion only if a reliable methodology was so altered as to skew the methodology itself." *United States v. Beasley*, 102 F.3d 1440, 1448 (8th Cir. 1996) (internal quotes and punctuation marks omitted); *United States v. Martinez*, 3 F.3d 1191, 1198 (8th Cir. 1993) ("Not every error in the application of a particular methodology should warrant exclusion. An alleged error in the application of a reliable methodology should provide the basis for exclusion of the opinion only if that error negates the basis for the reliability of the principle itself."). *See also Davis*, 602 F. Supp. 2d at 678 (same); *United States v. Williams*, 2008 WL 5382264, at *16 (C.D. Cal. 2008) ("*Daubert* concerns the methodology of the scientific evidence, and is not normally concerned with human error in applying the methodology.").

Ferdinand's authorities agree that, even under amended Rule 702, the Court's role is not to

determine whether an expert's conclusions are correct. In *Beasley*, for example, the Eighth Circuit cautioned that "alleged deficiencies [in the lab's protocols] go to the weight of the DNA evidence, not to its admissibility." 102 F.3d at 1448. There, the defendant alleged that the lab that did the DNA testing "did not observe (1) frequent external proficiency testing of personnel who perform DNA testing; (2) double blind external tests to check results and to show that proper procedures are being followed; and (3) maintaining records of errors in PCR testing." *Id.* None of the defendant's allegations suggested that the lab had so altered the PCR methodology as to make the test results inadmissible, however, so the trial court properly admitted the DNA evidence. *Id*. And in *Rudd v. Gen'l Motors Corp*., 127 F. Supp. 2d 1330, 1337 (M.D. Ala. 2001), the court noted that, even under the amended Rule 702, "the trial judge must still avoid usurping the role of the trier of fact." Quoting the Advisory Committee notes (which in turn quote *Daubert*), the court found that "vigorous cross-examination, presentation of contrary evidence, and careful instruction on the burden of proof are the traditional and appropriate means of attacking" even shaky evidence. Id. [4]

## III. CONCLUSION

For the foregoing reasons, the Court should deny Ferdinand's motion and admit the DNA evidence.

DATED: December 22, 2015

Respectfully submitted,

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/s/
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[4] It is significant that a more robust version of the instant motion was filed in this district a little over a year ago and was denied. *See United States v. Hayes*, CR 13-085, Docket Nos. 113-114. Unlike in this case, in *Hayes*, the defense submitted a declaration from Professor Inman challenging SERI's analysis. The arguments were considered and rejected by Judge Donato, who found the evidence to be both reliable and admissible. *See* Order, CR 13-085, Docket No. 134. The government respectfully submits that this Court should also deny the defendant's motion, which provides no basis to challenge the experts conclusions.